SUPPLEMENTAL TABLE 1

Two independent duplicate T_{50} values (°C) for parent CBH IIs, 23 original sample set CBH II chimeras and predicted thermostable CBH II chimeras. The 18 chimeras synthesized for this work are preceded by an asterisk.

Sample Set Chimeras & Parents				Predicted Thermostable Chimeras			
Sequence	$T_{50}(1)$	$T_{50}(2)$	MeanT_{50}	Sequence	$T_{50}(1)$	$T_{50}(2)$	MeanT_{50}
32333113	52	51	51.5	12332331	66.5	67	66.8
13111313	56	53.5	54.8	*13112332	67	67	67
11313121	55	55.5	55.3	22311331	68	68	68
21131311	57.5	57	57.3	*12111332	68	68	68
31212111	59	58	58.5	*12112332	68.5	67.5	68
Parent 2	**60**	**58**	**59**	12131331	68.5	69	68.8
23233133	61	61	61	*12131332	70	67.5	68.8
31311112	60	62	61	*12332332	69	69	69
22212231	63	61	62	12111131	70	68.5	69.3
13231111	63	6.5	63.3	12311332	70	69	69.5
12213111	63	63.5	63.3	13332331	70	69	69.5
Parent 3	**63.5**	**64.5**	**64**	12132331	70.5	69	69.8
12133333	64	64	64	*12132332	70.5	69	69.8
Parent 1	**64**	**65.5**	**64.8**	*13332332	69.5	70	69.8
33133132	65	66	65	12112132	71	68.5	69.8
11332333	64.5	66	65.3	13322332	71	68.5	69.8
23311333	65	66	65.5	*13131332	70	70	70
33213332	66	66	66	*12331332	71	69	70
13333232	67.5	67	67.3	*13312332	70	70	70
22232132	68	68	68	*11113332	69.5	70.5	70
11113132	71.5	71	71.3	*13113132	70.5	69.5	70
21333331	73.5	75.5	74.5	*11112132	70.5	70	70.3
21311131	75.5	75.5	75	*12113132	70.5	70.5	70.5
				*13132332	69.5	71.5	70.5
				*11111132	71	70.5	70.8
				13331332	72	70	71
				*13111132	72	69.5	71.3
				*12222132	72.5	70	71.3
				12222332	72	69.5	71.3
				13311332	71	71.5	71.7
				13311331	73.5	72.5	73

SUPPLEMENTAL TABLE 2

Amino acid sequences for CBH II parent and chimera catalytic domains shown in Supplemental Table 1. Table also includes catalytic domain for *P. chrysosporium* CBH II as described in text. All recombinant CBH IIs share the N-terminal CBM and linker from the native *H. jecorina* CBH II, CSSVWGQCGGQNWSGPTCCASGSTCVYSNDYYSQCLPGAASSSSSTRAASTTSRVSPTTSRSSSA TPPPGSTTTRVPPVGSGTATYS.

Parent 1 (*H. insolens*)
GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLLVQTLSE
IREANQAGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREILISFSDVRT
ILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQ
PAAELFAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEARGF
P_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDGTS
DTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

Parent 2 (*H. jecorina*)
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFMWLDT_LDKTPLMEQTLA
DIRTANKNGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDTIRQIVVEYSDIR
TLLVIEPDSLANLVTNLGTPKCANAQSAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQ
DPAAQLFANVYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNAVYNEKLYIHAIGPLLANH
GWSNAFFITDQGRSGKQPTGQQQWGDWCNVIGTGFGIRPSANTGDSLLDSFVWVKPGGECDGT
SDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

Parent 3 (*C. thermophilum*)
GNPFSGVQLWANTYYSSEVHTLAIPSLS_PELAAKAAKVAEVPSFQWLDRNVTVDTLFSGTLAEI
RAANQRGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIRELLIQYSDIRTI
LVIEPDSLANMVTNMNVQKCSNAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDTSAARYDYHCGLSDALTPAPEAGQWFQAYFEQLLINANPPF_

P. chrysosporium CBH II
NNPWTGFQIFLSPYYANEVAAAA_KQITDPTLSSKAASVANIPTFTWLDSVAKIPDLGTYLASASA
LGKSTGT__KQLVQIVIYDLPDRDCAAKASNGEFSIANNGQANYENYIDQIVAQIQQFPDVRVVA
VIEPDSLANLVTNLNVQKCANAKTTYLACVNYALTNLAKVGVYMYMDAGHAGWLGWPANLS
PAAQLFTQVWQNAGKSPFIKGLATNVANYNALQAASPDPITQGNPNYDEIHYINALAPLLQQAG
WD_ATFIVDQGRSGVQNIRQ_QWGDWCNIKGAGFGTRPTTNTGSQFIDSIVWVKPGGECDGTSN
SSSPRYDSTCSLPDAAQPAPEAGTWFQAYFQTLVSAANPPL_

32333113
GNPFSGVQLWANTYYSSEVHTLAIPSLS_PELAAKAAKVAEVPSFMWLDT_LDKTPLMEQTLADI
RTANKNGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIRELLIQYSDIRTI
LVIEPDSLANMVTNMNVQKCSNAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEAR
GFP_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDG
TSDTSAARYDYHCGLSDALTPAPEAGQWFQAYFEQLLINANPPF_

13111313
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ILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQ
PAAELFAKIYEDAGKPRAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQGF
D_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDGTS
DTSAARYDYHCGLSDALTPAPEAGQWFQAYFEQLLINANPPF_

11313121
GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLLVQTLSE
IREANQAGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIREILISFSDVRTI
LVIEPDSLANMVTNMNVPKCSGAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEAR
GFPNAFFITDQGRSGKQPTGQQQWGDWCNVIGTGFGIRPSANTGDSLLDSFVWVKPGGECDGTS
DTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

21131311
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFQWLDRNVTVDTLLVQTLS
EIREANQAGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIRELLIQYSDI
RTILVIEPDSLANMVTNMNVQKCSNAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPA
NIQPAAELFAKIYEDAGKPRAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRN
QGFD_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECD
GTSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

31212111
GNPFSGVQLWANTYYSSEVHTLAIPSLS_PELAAKAAKVAEVPSFQWLDRNVTVDTLLVQTLSEI
REANQAGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDRIREILISFSDVRTIL
VIEPDSLANMVTNMNVPKCSGAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQDP
AAQLFANVYKNASSPRALRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEARGF
P_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDGTS
DTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

23233133
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFQWLDRNVTVDTLFSGTLA
EIRAANQRGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDRIRELLIQYSDIR
TILVIEPDSLANMVTNMNVQKCSNAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPA
NIQPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEA
RGFP_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESD
GTSDTSAARYDYHCGLSDALTPAPEAGQWFQAYFEQLLINANPPF

31311112
GNPFSGVQLWANTYYSSEVHTLAIPSLS_PELAAKAAKVAEVPSFQWLDRNVTVDTLLVQTLSEI
REANQAGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIREILISFSDVRTIL
VIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQP
AAELFAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEARGFP
_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDGTSD
SSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

22212231
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFMWLDT_LDKTPLMEQTLA
DIRTANKNGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDRIREILISFSDVR
TILVIEPDSLANMVTNMNVPKCSGAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPAN

QDPAAQLFANVYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNAVYNEKLYIHAIGPLLAN
HGWS_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESD
GTSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

13231111
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IRAANQRGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDRIRELLIQYSDIRTI
LVIEPDSLANMVTNMNVQKCSNAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQ
PAAELFAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEARGF
P_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDGTS
DTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

12213111
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IRTANKNGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDRIREILISFSDVRTI
LVIEPDSLANMVTNMNVPKCSGAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEAR
GFP_AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDG
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12133333
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IRTANKNGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIRELLIQYSDIR
TILVIEPDSLANMVTNMNVQKCSNAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPA
NIQPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRN
QGFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESD
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33133132
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RAANQRGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIRELLIQYSDIRT
ILVIEPDSLANMVTNMNVQKCSNAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEAR
GFP_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

11332333
GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLLVQTLSE
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LVIEPDSLANMVTNMNVQKCSNAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQ
DPAAQLFANVYKNASSPRALRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDTSAARYDYHCGLSDALTPAPEAGQWFQAYFEQLLINANPPF_

23311333
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFQWLDRNVTVDTLFSGTLA
EIRAANQRGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIREILISFSDVR
TILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANI
QPAAELFAKIYEDAGKPRAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ

GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDTSAARYDYHCGLSDALTPAPEAGQWFQAYFEQLLINANPPF_

33213332
GNPFSGVQLWANTYYSSEVHTLAIPSLS_PELAAKAAKVAEVPSFQWLDRNVTVDTLFSGTLAEI
RAANQRGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDRIREILISFSDVRTI
LVIEPDSLANMVTNMNVPKCSGAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

13333232
GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLFSGTLAE
IRAANQRGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIRELLIQYSDIRTI
LVIEPDSLANMVTNMNVQKCSNAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNGWNITSPPSYTQGNAVYNEKLYIHAIGPLLANH
GWS_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

22232132
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFMWLDT_LDKTPLMEQTLA
DIRTANKNGGN__YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDRIRELLIQYSDIR
TILVIEPDSLANMVTNMNVQKCSNAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPAN
QDPAAQLFANVYKNASSPRALRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEA
RGFP_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESD
GTSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

11113132
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ILVIEPDSLANMVTNMNVPKCSGAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPANI
QPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEAR
GFP_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

21333331
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TILVIEPDSLANMVTNMNVQKCSNAASTYKELTVYALKQLNLPHVAMYMDAGHAGWLGWPA
NIQPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRN
QGFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESD
GTSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

21311131
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFQWLDRNVTVDTLLVQTLS
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ILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQ
PAAELFAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEARGF
P_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDGTS
DTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

12332331
GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFMWLDT_LDKTPLMEQTLAD
IRTANKNGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIRELLIQYSDIRTI
LVIEPDSLANMVTNMNVQKCSNAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQ
DPAAQLFANVYKNASSPRALRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

13112332
GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLFSGTLAE
IRAANQRGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREILISFSDVRT
ILVIEPDSLANMVTNMNVPKCSGAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQ
DPAAQLFANVYKNASSPRALRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

22311331
GNPFVGVTPWANAYYASEVSSLAIPSLT_GAMATAAAAVAKVPSFMWLDT_LDKTPLMEQTLA
DIRTANKNGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIREILISFSDVR
TILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANI
QPAAELFAKIYEDAGKPRAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

12111332
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IRTANKNGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREILISFSDVRT
ILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQ
PAAELFAKIYEDAGKPRAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQGF
D_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDGTS
DSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

12112332
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IRTANKNGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREILISFSDVRT
ILVIEPDSLANMVTNMNVPKCSGAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQ
DPAAQLFANVYKNASSPRALRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

12131331
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IRTANKNGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIRELLIQYSDIR
TILVIEPDSLANMVTNMNVQKCSNAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANI
QPAAELFAKIYEDAGKPRAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF_

12131332
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TILVIEPDSLANMVTNMNVQKCSNAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANI
QPAAELFAKIYEDAGKPRAVRGLATNVANYNAWSIASPPSYTSPNPNYDEKHYIEAFAPLLRNQ
GFD_AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGHELVDAFVWVKPGGESDG
TSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

12332332
GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFMWLDT_LDKTPLMEQTLAD
IRTANKNGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIRELLIQYSDIRTI
LVIEPDSLANMVTNMNVQKCSNAASAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQ
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SUPPLEMENTAL TABLE 3

T_{50} linear regression model parameters and p-values. Parameter values with $p \leq 0.1$, used to calculate the regression fit line of Figure 1, appear in bold. Block effects are reported relative to a parent 1 (*H. insolens* CBH II) reference state with 16 parameters representing substitution of each of the 8 blocks from parents 2 and 3.

Block	Parameter Value	p-value
Parent1	**62.8**	**0.00**
B12	-0.9	0.35
B13	**-3.5**	**0.00**
B22	**-1.7**	**0.06**
B23	-1.1	0.25
B32	0.5	0.68
B33	**1.2**	**0.10**
B42	**2.7**	**0.05**
B43	0.0	0.99
B52	**-1.3**	**0.10**
B53	-0.6	0.50
B62	**-3.5**	**0.02**
B63	-0.7	0.37
B72	**-3.8**	**0.05**
B73	**8.5**	**0.00**
B82	0.0	1.00
B83	**-5.6**	**0.00**

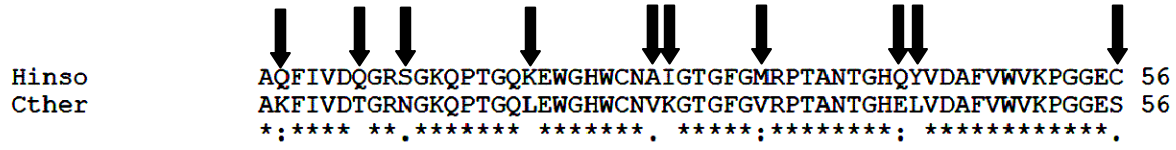
SUPPLEMENTAL TABLE 4

Total activity in synthetic (SDCAA) and rich (YPD) expression culture media supernatants for *H. jecorina* and *H. insolens* wild type, Ser point mutant and B7P3 block substitution CBH IIs. Values presented are μg glucose/mL cellulase activity assay per mL of expression culture supernatant CBH II equivalent added to cellulase activity assay. For SDCAA cultures, concentrated SDCAA culture supernatants were used and activity toward phosphoric acid swollen cellulose (1 mg/mL) at 50 °C for 100 minutes in 50 mM sodium acetate, pH 4.8, was measured. YPD supernatant CBH II was concentrated by binding to Avicel and activity toward Avicel (15 mg/mL) at 55 °C for 150 minutes in 50 mM sodium acetate, pH 4.8, was measured.

CBH II	SDCAA (1)	SDCAA (2)	SDCAA Mean	YPD (1)	YPD (2)	YPD Mean
H. jecorina	19	17	18	0.4	0.4	0.4
H. jeco C311S	50	43	47	6.1	5.6	5.9
H. jeco B7P3	35	33	34	3.9	3.6	3.8
H. insolens	73	83	78	6.2	6.0	6.1
H. inso C314S	100	97	98	8.8	8.0	8.4
H. inso B7P3	39	42	40	4.4	4.1	4.2

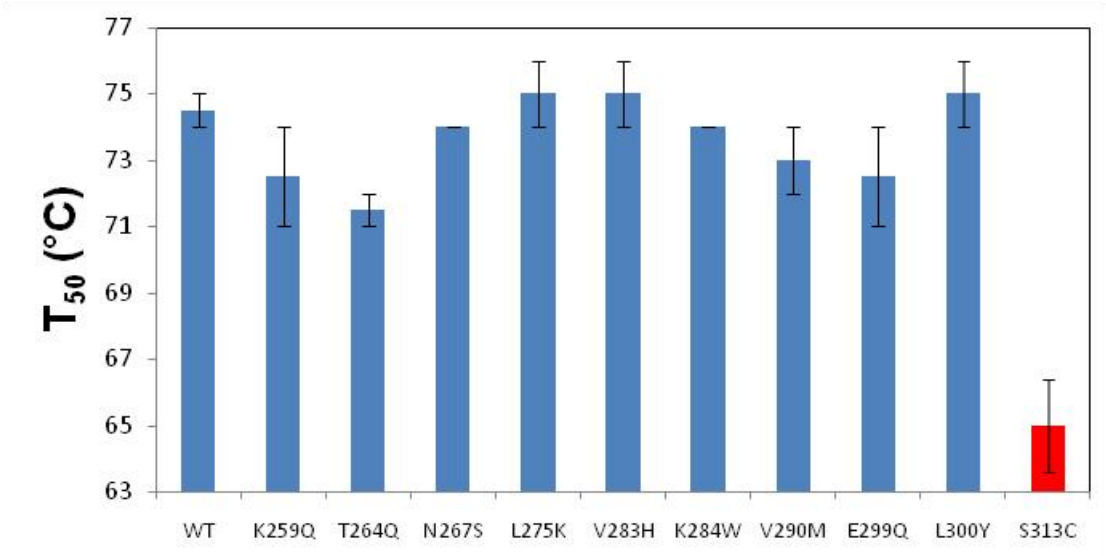
SUPPLEMENTAL FIGURE 1

ClustalW multiple sequence alignment for block 7 from parent 1, *H. insolens* and parent 3, *C.thermophilum*. Arrows denote residues changed in reversion mutants.



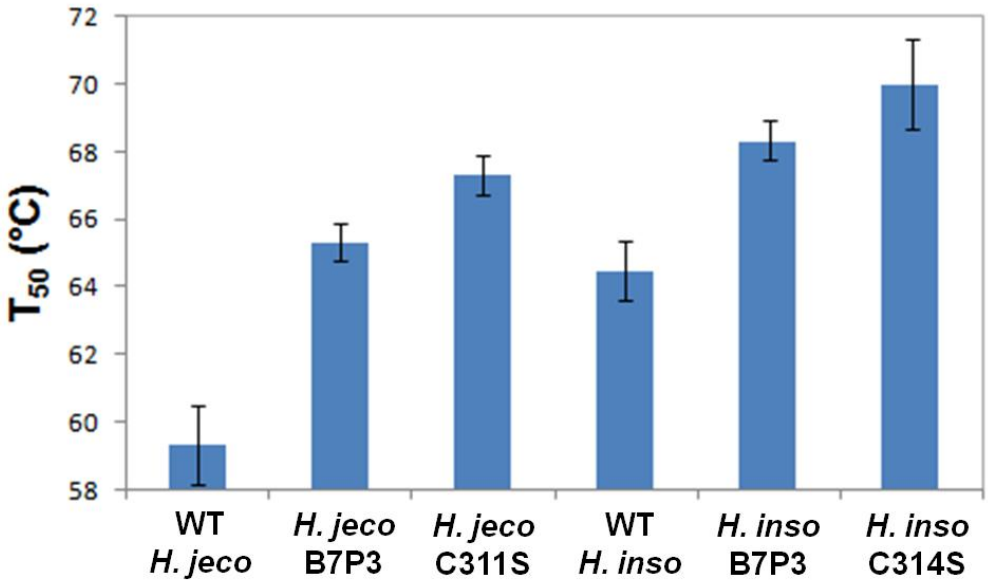
SUPPLEMENTAL FIGURE 2

T_{50} values for 21111331 chimera point mutants. Values shown as average of two independent duplicates, error bars indicate duplicate T_{50} values for each point mutant. Inactivation was carried out for 10 minutes at the temperature being tested in 50 mM sodium acetate buffer, pH 4.8. Residual activity was determined by incubation with 1 g/L phosphoric acid swollen cellulose (PASC) in above buffer for 100 minutes at 50 °C.



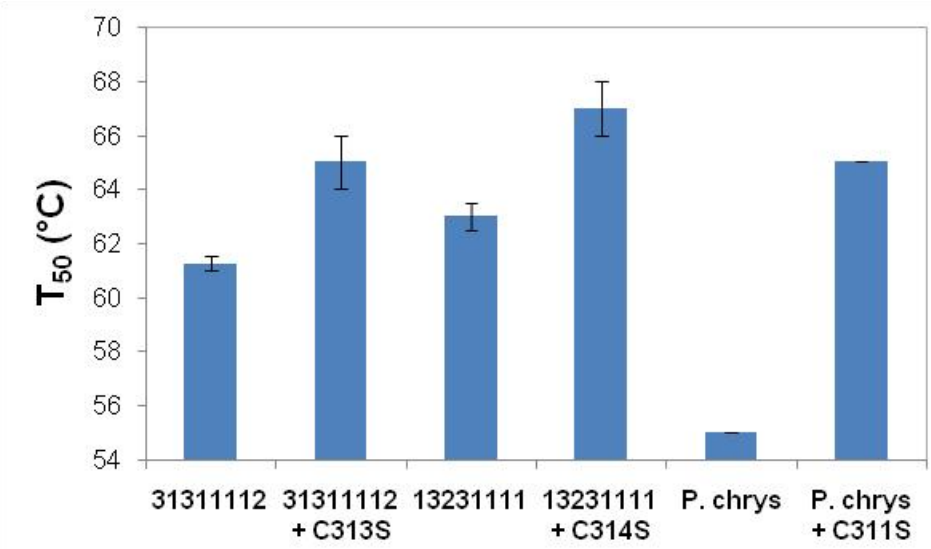
SUPPLEMENTAL FIGURE 3

T_{50} values for *H. insolens* and *H. jecorina* parent CBH IIs, Ser single point mutants and B7P3 block substitution chimeras. Values shown as average of three independent replicates, error bars indicate one standard deviation for each CBH II. Inactivation was carried out for 10 minutes at the temperature being tested in 50 mM sodium acetate buffer, pH 4.8. Residual activity was determined by incubation with 1 g/L phosphoric acid swollen cellulose (PASC) in above buffer for 100 minutes at 50 °C.



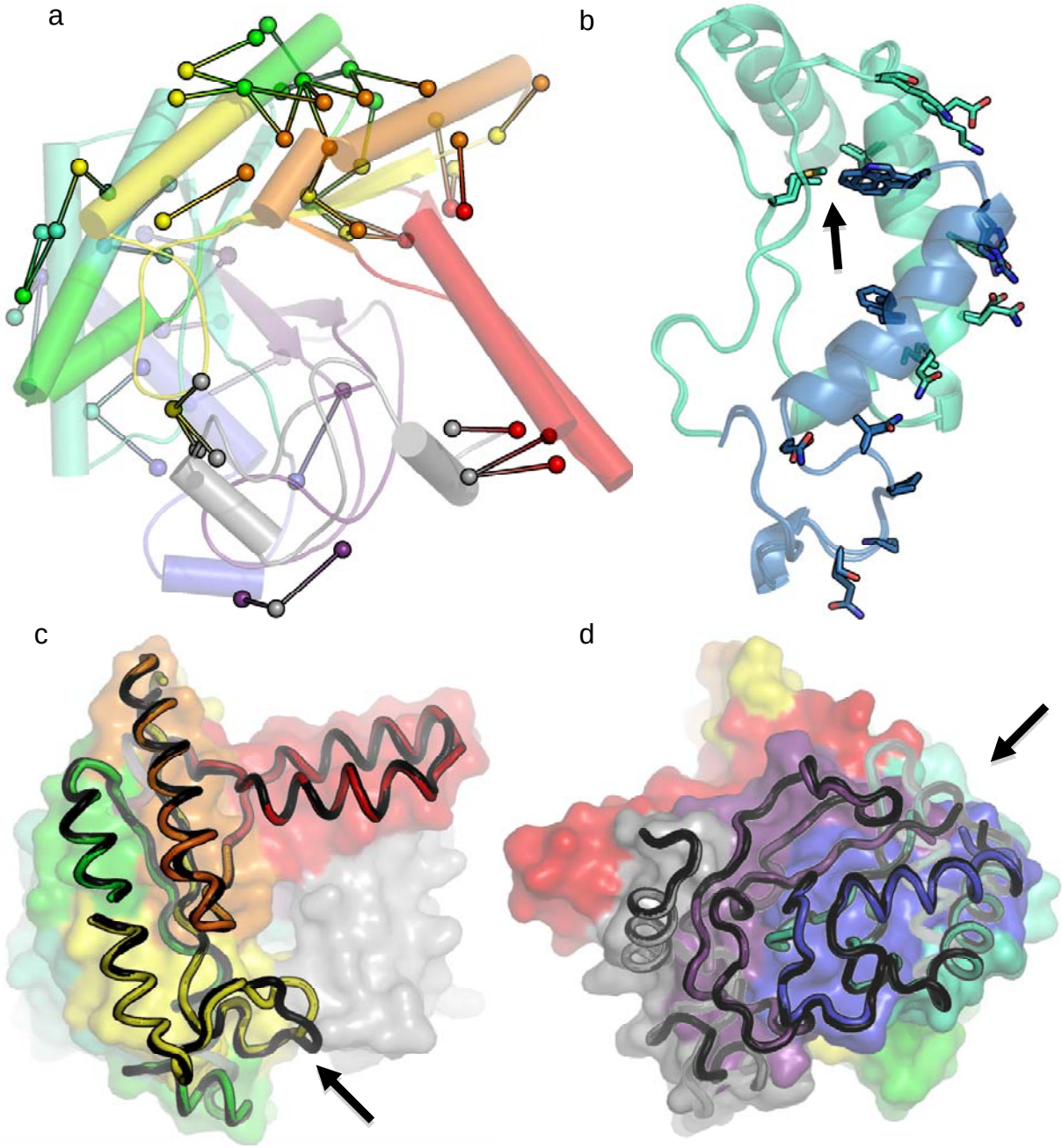
SUPPLEMENTAL FIGURE 4

T_{50} values for CBH II chimeras 31311112, 13231111 and the wild type CBH II catalytic domain from *P. chrysosporium* (fused to the *H. jecorina* CBM) and heterologously secreted from *S. cerevisiae*. Values shown as two independent replicates with error bars indicating values for each trial. Inactivation was carried out for 10 minutes at the temperature tested, in 50 mM sodium acetate buffer, pH 4.8. Residual activity was determined by incubation with 1 g/L phosphoric acid swollen cellulose (PASC) in above buffer for 100 minutes at 50 °C.



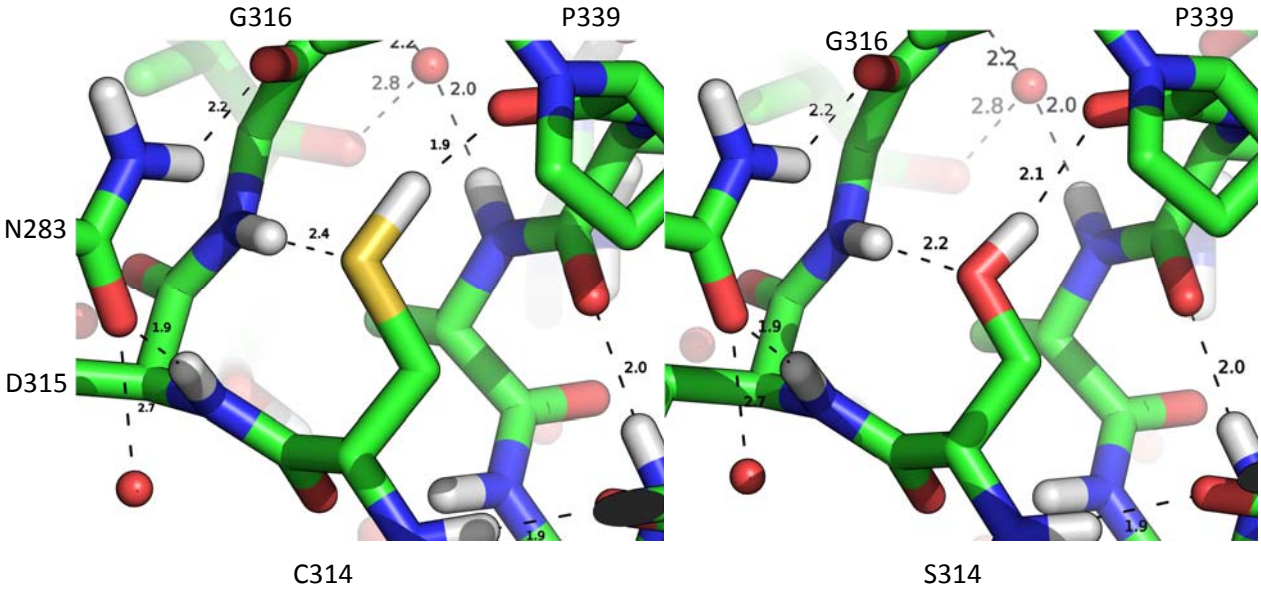
SUPPLEMENTAL FIGURE 5

CBH II recombination block interfaces. (a) Inter-block sites where novel non-parental residue pairs are possible (connected spheres) are usually surface-exposed, potentially allowing solvent to screen the interactions. (b) An example interface (B5-B6) illustrates conservation of the backbone (cartoons for aligned *H. jecorina* and *H. insolens*), variable residues on the surface, and the comparatively rare possibility of a novel buried hydrophobic pair at residues 173 and 253 (arrow). (c) Blocks 1-4 from *H. jecorina* (black cartoon) match cognate *H.insolens* blocks (color-coded cartoon) without large deviations, though movement associated with substrate binding is observed (arrow) in part of B3 (yellow). (d) Cognate blocks 5-8 are also similar, though the indel at the B6,B7 junction (arrow) will require conformational change.


a
b
c
d

SUPPLEMENTAL FIGURE 6

Structural analysis of C314S mutation and its stabilizing effect. (a) Hydrogen positions for high-resolution *H.insolens* structure (1ocn) were added with REDUCE.[1] (b) The reconfigured geometry of the analogous serine structure was modeled in PyMOL (http://www.pymol.org). Sidechain optimization in the SHARPEN[2] modeling platform (with an all-atom Rosetta energy function) also suggested that both the Cys314 and Ser314 would donate hydrogen bonds to the carbonyl of Pro339, and accept hydrogen bonds from the amide of Gly316. The superior hydrogen bonding capacity of serine may play a role in the greater stability of the serine containing variants. Another possible explanation is geometric complementarity. Specifically, the Cys position from 1ocn shows evidence of conformational strain in that the sidechain is noticeably bent (i.e. the improper dihedral angle from N-C-Cα-Cβ is 6° from the standard position), increasing the distance from the Pro carbonyl. Numbers in figure not preceded by letters denote hydrogen bond distances (Å).



SUPPLEMENTAL FIGURE 7

Alignment of 60 amino acid frame bracketing *H. jecorina* CBH II Cys311 for 196 protein sequences having highest identity to *H. jecorina* CBH II. Residues at 311 equivalent position denoted by shaded bar. Sequences for recombinant *C. thermophilum*, *H. insolens* and *P. chrys* CBH IIs studied in this work are denoted as *C. ther*, *H. inso* and *P. chrys*. Fifty-four of the 250 most identical sequences were excluded due to redundancy (i.e. point mutants for structural studies or >95% identical isoforms).

```
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XP_001552807    ----T---G---D----A---L--EDAFVWIKPGGEGDG--T----S-------------
XP_001216114    ----T---G---N----S---L--VDAFVWVKPGGESDG--T----S-------------
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XP_002380541    ----T---G---D----E---L--VDAFVWVKPGGESDG--T----S-------------
AAQ72468        ----T---G---D----A---L--VDAFVWVKPGGESDG--T----S-------------
P46236          ----T---G---D----A---L--ADAFVWVKPGGESDG--T----S-------------
XP_001903170    ----T---G---L----D---I--EDAFVWIKPGGECDG--T----S-------------
JC7931          ----T---G---N----P---L--EDAFVWVKPGGESDG--T----S-------------
XP_001273717    ----T---G---D----D---L--LDAFVWVKPGAESDG--T----S-------------
XP_001210279    ----T---G---D----E---L--VDAFVWVKPGGESDG--T----S-------------
XP_002484367    ----T---G---D----P---L--EDAFVWVKPGGESDG--T----S-------------
XP_001264772    ----T---G---D----K---L--VDAFVWVKPGGESDG--T----S-------------
XP_960770       ----T---G---S----S---L--ADAFVWVKPGGESDG--T----S-------------
XP_658877       ----T---G---D----E---L--VDAFVWVKPGGESDG--T----S-------------
ACH91035        ----T---G---D----P---L--EDAFVWVKPGGESDG--T----S-------------
XP_001226029    ----T---G---H----D---L--LDAFVWIKPGGECDG--T----S-------------
XP_360146       ----T---G---S----E---L--ADAFVWIKPGGECDG--V----S-------------
C.ther          ----T---G---H----E---L--VDAFVWVKPGGESDG--T----S-------------
XP_002149891    ----T---G---D----P---L--EDAFVWVKPGGESDG--T----S-------------
XP_001269265    ----T---G---D----E---L--VDAFVWVKPGGESDG--T----S-------------
H.inso          ----T---G---H----Q---Y--VDAFVWVKPGGECDG--T----S-------------
XP_001598803    ----T---G---D----A---L--EDAFVWVKPGGEADG--T----S-------------
AAM76664        ----T---G---N----A---L--IDAIVWVKPGGESDG--T----S-------------
XP_001933777    ----T---G---N----A---N--VDAFVWVKPGGESDG--T----S-------------
XP_001796781    ----T---D---D----P---L--LDAYVWVKPGGEGDG--T----S-------------
AAA50608        ----T---G---S----S---L--IDAIVWVKPGGECDG--T----S-------------
AAK28357        ----T---G---S----S---L--IDSIVWVKPGGECDG--T----S-------------
BAF80327        ----T---G---S----S---L--IDAIVWVKPGGESDG--T----S-------------
XP_001792324    ----T---G---N----S---L--VDALVWVKPGGESDG--T----S-------------
BAG48183        ----T---G---S----S---L--IDSIVWVKPGGESDG--T----S-------------
BAH59082        ----T---G---S----P---L--IDSIVWVKPGGECDG--T----S-------------
AAT64008        ----T---G---S----S---L--IDAIVWIKPGGECDG--T----T-------------
P.crys          ----T---G---S----Q---F--IDSIVWVKPGGECDG--T----S-------------
BAH59083        ----T---P---S----S---L--IDSIVWVKPGGEADG--T----S-------------
XP_001833045    ----T---P---S----S---A--IDAIVWIKPGGEADG--T----S-------------
AAF35251        ----T---G---N----P---L--IDAIIWVKPGGESDG--T----S-------------
XP_001226566    ----T---G---A----D---L--ADAFVWVKPGGESDG--T----S-------------
XP_001903893    ----T---G---L----E---L--ADAFVWVKPGGESDG--T----S-------------
XP_002391276    ----T---G---S----S---L--IDSIVWVKPGGE--------------------------
XP_956581       ----T---G---H----D---L--ADAFVWVKPGGESDG--T----S-------------
XP_362054       ----T---G---S----S---L--TDALLWVKPGGESDG--T----S-------------
XP_001806560    ----T---G---N----T---L--VDAFVWVKPGGESDG--T----S-------------
XP_001931623    ----W---G---D----C---L--VDSFVWGKPGGESDG--T----S-------------
AAL15038        ----T---G---S----S---L--IDAIVWVKPGGESDG--T----S-------------
AAL01211        ----P---I---S----S---MDYLDAFYWIKPLGESDG--T----S-------------
XP_001839612    ----QRILN---N----T---N--VDAIVWVKPGGESDG--T----S-------------
AAL92497        ----S---G---M----D---Y--LDAFYWVKPLGESDG--Y----S-------------
YP_001618727    ----P---G---G----A---TN-LDAFVWVKPPGDSDG--V----G-------------
AAM94167        ----S---G---M----D---Y--LDAFYWVKPYGESDG--T----S-------------
XP_001836853    ----Q---GVLQN----P---N--VDAIVWVKPGGESDG--T----S-------------
AAL01212        ----S---G---M----D---Y--LDAFYWIKPLGESDG--T----S-------------
XP_001841133    ----L---D---S----E---N--VDAIVWVKPGGESDG--T----S-------------
XP_001841132    ----Q---AIV-D----S---AN-VDAIVWVKPGGESDG--T----S-------------
AAP30749        ----A---G---M----D---Y--LDAFYWVKPYGESDG--T----S-------------
XP_001224490    ----T---N---N----T---V--VDALVWVKPGGESDG----------------------
XP_368004       ----T---E---N----P---H--VDSIVWVKPGGESDG----------------------
XP_001903209    ----T---N---N----T---V--VDAIVWIKPGGESDG----------------------
AAD51055        ----P---D---S----SKP-L--LDAYMWIKTPGEADG--S----S-------------
XP_001226518    ----T---G---N----N---N--VDAIVWIKPGGESDG----------------------
XP_957415       ----Q---SVLQN----S---N--VDAIVWIKPGGESDG----------------------
ABY52798        ----S---G---Y----P---L--LDAFMWLKTPGEADG--S----A-------------
XP_001795501    ----T---N---N----T---H--IDSIVWIKPGGESDG--A-------------------
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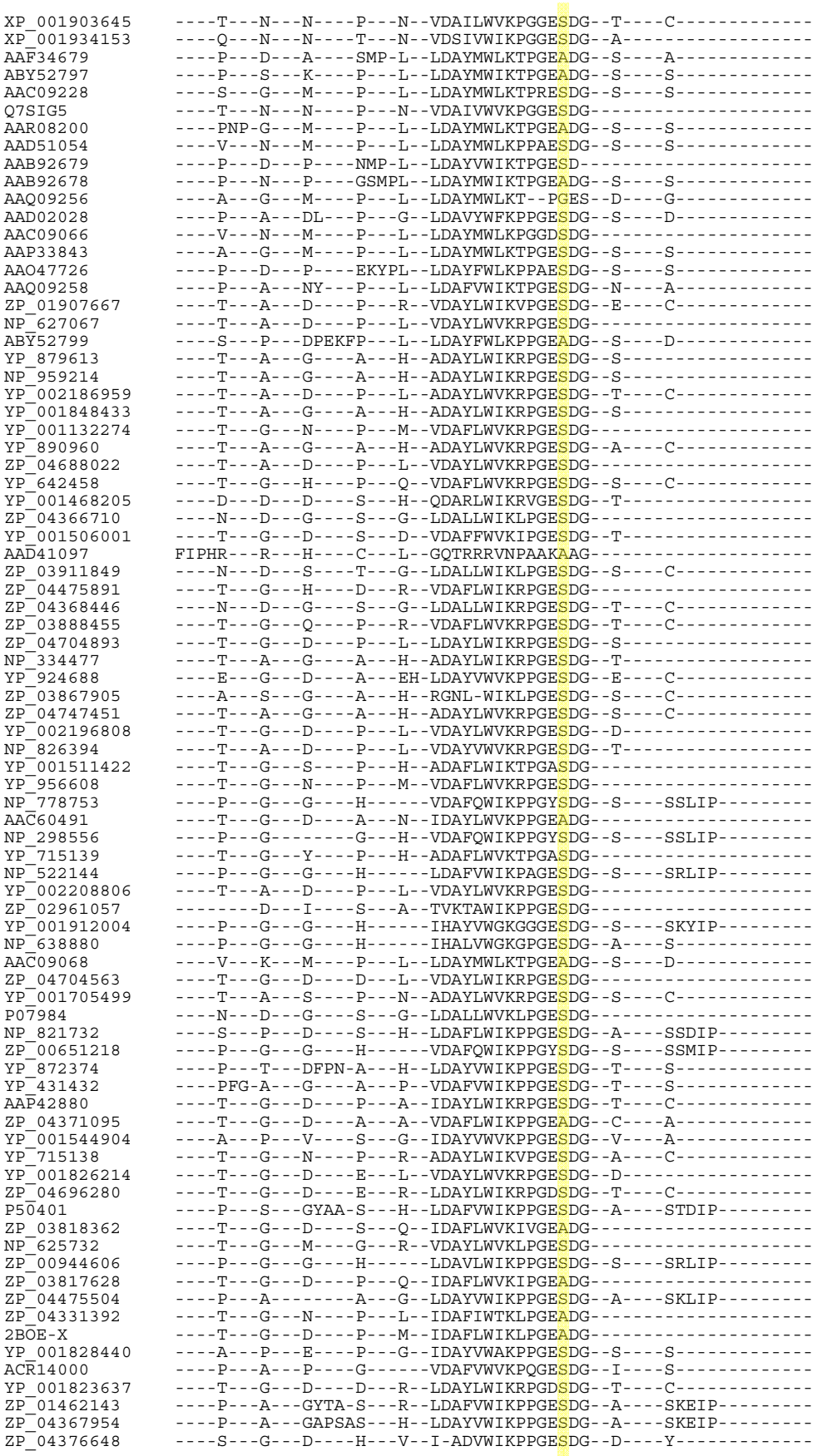
XP_001903645 ----T---N---N----P---N--VDAILWVKPGGESDG--T----C----------
XP_001934153 ----Q---N---N----T---N--VDSIVWIKPGGESDG--A----------------
AAF34679 ----P---D---A----SMP-L--LDAYMWLKTPGEADG--S----A----------
ABY52797 ----P---S---K----P---L--LDAYMWIKTPGEADG--S----S----------
AAC09228 ----S---G---M----P---L--LDAYMWLKTPRESDG--S----S----------
Q7SIG5 ----T---N---N----P---N--VDAIVWVKPGGESDG----------
AAR08200 ----PNP-G---M----P---L--LDAYMWLKTPGEADG--S----S----------
AAD51054 ----V---N---M----P---L--LDAYMWLKPPAESDG--S----S----------
AAB92679 ----P---D---P----NMP-L--LDAYVWIKTPGESD----------
AAB92678 ----P---N---P----GSMPL--LDAYMWIKTPGEADG--S----S----------
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AAD02028 ----P---A---DL---P---G--LDAVYWFKPPGESDG--S----D----------
AAC09066 ----V---N---M----P---L--LDAYMWLKPGGDSDG----------
AAP33843 ----A---G---M----P---L--LDAYMWLKTPGESDG--S----S----------
AAO47726 ----P---D---P----EKYPL--LDAYFWLKPPAESDG--S----S----------
AAQ09258 ----P---A---NY---P---L--LDAFVWIKTPGESDG--N----A----------
ZP_01907667 ----T---A---D----P---R--VDAYLWIKVPGESDG--E----C----------
NP_627067 ----T---A---D----P---L--VDAYLWVKRPGESDG----------
ABY52799 ----S---P---DPEKFP---L--LDAYFWLKPPGEADG--S----D----------
YP_879613 ----T---A---G----A---H--ADAYLWIKRPGESDG--S----------
NP_959214 ----T---A---G----A---H--ADAYLWIKRPGESDG--S----------
YP_002186959 ----T---A---D----P---L--ADAYLWVKRPGESDG--T----C----------
YP_001848433 ----T---A---G----A---H--ADAYLWIKRPGESDG--S----------
YP_001132274 ----T---G---N----P---M--VDAFLWVKRPGESDG----------
YP_890960 ----T---A---G----A---H--ADAYLWVKRPGESDG--A----C----------
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YP_642458 ----T---G---H----P---Q--VDAFLWVKRPGESDG--S----C----------
YP_001468205 ----D---D---D----S---H--QDARLWIKRVGESDG--T----------
ZP_04366710 ----N---D---G----S---G--LDALLWIKLPGESDG----------
YP_001506001 ----T---G---D----S---D--VDAFFWVKIPGESDG--T----------
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ZP_03911849 ----N---D---S----T---G--LDALLWIKLPGESDG--S----C----------
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ZP_04368446 ----N---D---G----S---G--LDALLWIKRPGESDG--T----C----------
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ZP_04704893 ----T---G---D----P---L--LDAYLWIKRPGESDG--S----------
NP_334477 ----T---A---G----A---H--ADAYLWIKRPGESDG--T----------
YP_924688 ----E---G---D----A---EH-LDAYVWVKPPGESDG--E----C----------
ZP_03867905 ----A---S---G----A---H--RGNL-WIKLPGESDG--S----C----------
ZP_04747451 ----T---A---G----A---H--ADAYLWVKRPGESDG--S----C----------
YP_002196808 ----T---G---D----P---L--VDAYLWVKRPGESDG--D----------
NP_826394 ----T---A---D----P---L--VDAYVWVKRPGESDG--T----------
YP_001511422 ----T---G---S----P---H--ADAFLWIKTPGASDG----------
YP_956608 ----T---G---N----P---M--VDAFLWVKRPGESDG----------
NP_778753 ----P---G---G----H------VDAFQWIKPPGYSDG--S----SSLIP---------
AAC60491 ----T---G---D----A---N--IDAYLWVKPPGEADG----------
NP_298556 ----P---G--------G---H--VDAFQWIKPPGYSDG--S----SSLIP---------
YP_715139 ----T---G---Y----P---H--ADAFLWVKTPGASDG----------
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YP_001912004 ----P---G---G----H------IHAYVWGKGGGESDG--S----SKYIP---------
NP_638880 ----P---G---G----H------IHALVWGKGPGESDG--A----S----------
AAC09068 ----V---K---M----P---L--LDAYMWLKTPGEADG--S----D----------
ZP_04704563 ----T---G---D----D---L--VDAYLWIKRPGESDG----------
YP_001705499 ----T---A---S----P---N--ADAYLWVKRPGESDG--S----C----------
P07984 ----N---D---G----S---G--LDALLWVKLPGESDG----------
NP_821732 ----S---P---D----S---H--LDAFLWIKPPGESDG--A----SSDIP---------
ZP_00651218 ----P---G---G----H------VDAFQWIKPPGYSDG--S----SSMIP---------
YP_872374 ----P---T---DFPN-A---H--LDAYVWIKPPGESDG--T----S----------
YP_431432 ----PFG-A---G----A---P--VDAFVWIKPPGESDG--T----S----------
AAP42880 ----T---G---D----P---A--IDAYLWIKRPGESDG--T----C----------
ZP_04371095 ----T---G---D----A---A--VDAFLWIKPPGEADG--C----A----------
YP_001544904 ----A---P---V----S---G--IDAYVWVKPPGESDG--V----A----------
YP_715138 ----T---G---N----P---R--ADAYLWIKVPGESDG--A----C----------
YP_001826214 ----T---G---D----E---L--VDAYLWVKRPGESDG--D----------
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P50401 ----P---S---GYAA-S---H--LDAFVWIKPPGESDG--A----STDIP---------
ZP_03818362 ----T---G---D----S---Q--IDAFLWVKIVGEADG----------
NP_625732 ----T---G---M----G---R--VDAYLWVKLPGESDG----------
ZP_00944606 ----P---G---G----H------LDAVLWIKPPGESDG--S----SRLIP---------
ZP_03817628 ----T---G---D----P---Q--IDAFLWVKIPGEADG----------
ZP_04475504 ----P---A--------A---G--LDAYVWIKPPGESDG--A----SKLIP---------
ZP_04331392 ----T---G---N----P---L--IDAFIWTKLPGEADG----------
2BOE-X ----T---G---D----P---M--IDAFLWIKLPGEADG----------
YP_001828440 ----A---P---E----P---G--IDAYVWAKPPGESDG--S----S----------
ACR14000 ----P---A---P----G------VDAFVWVKPQGESDG--I----S----------
YP_001823637 ----T---G---D----D---R--LDAYLWIKRPGDSDG--T----C----------
ZP_01462143 ----P---A---GYTA-S---R--LDAFVWIKPPGESDG--A----SKEIP---------
ZP_04367954 ----P---A---GAPSAS---H--LDAYVWIKPPGESDG--A----SKEIP---------
ZP_04376648 ----S---G---D----H---V--I-ADVWIKPPGESDG--D----Y----------

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YP_001902424    ----P---G--------A---H--LDAYAWVKPPGESDG--S----STLIP---------
ZP_03868469     ----P---T---DFPN-S---H--LDAYVWVKPPGESDG--S----SSEIP---------
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ZP_03912473     ----S---G---Y----P---H--IDAFVWVKPPGESDG--S----STEIP---------
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ZP_04707051     ----T---G---E----A---R--IDAYLWVKLPGESDG--C----S-------------
ZP_04482497     ----A---P---E----S---G--IDAYVWMKPPGESDG--S----SKEIP---------
BAB83928        ----P---A--------S---G--IDAYTWIKPPGESDG--N----SAPVD---------
ZP_04684292     ----G---G---A----E---M--L---LWIKVPGESDG--NCGVGA-------------
YP_002196127    ----P-------E----A---G--IDAYLWVKPPGESDG--S----SSEIP---------
P33682          ----G---G---A----E---M--L---LWIKTPGESDG--NCGVGS-------------
NP_823029       ----P---A--------T---G--IDAYVWMKPPGESDG--S----S-------------
NP_828072       ----T---G---E----A---G--IDAYLWVKLPGESDG----------------------
P26414          ----T---G---D----P---A--IDAFLWIKPPGEADG----------------------
YP_925799       ----V---F---D----G---A--FDGTLWVKHPGESDG--T----K-------------
ZP_04370960     ----G---A---S----N---H--IIAYVWIKPPGESDG--D----Y-------------
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ACR12723        ----P---S---P----G------IDAYVWVKPQGESDG--V----S-------------
ZP_04333277     ----A---P---E----A---G--IDAYVWMKPPGESDG--S----S-------------
ZP_04483608     ----V---G---E----G---A--QDARIWIKVPGDSDG----------------------
ZP_03390825     ----T---T---G----A---H--ADAYLWINGGGGSDG--E----C-------------
ZP_04377655     ----T---T---G----A---H--ADAYLWINGGGGSDG--E----C-------------
YP_001108158    ----G---G---A----D---L--L---VWAKVPGDSDG----------------------
ZP_04377654     ----T---T---G----A---H--ADAYLWINGGGGSDG--E----C-------------
ZP_04058051     ----T---T---G----A---H--ADAYLWINGGGGSDG--E----C-------------
YP_002203140    ----P---A--------A---G--IDAYVWIKPPGESDG--A----SSAVP---------
YP_632998       ----V---G---G----A---E--MT--LWIKVPGDSDG----------------------
ZP_04684732     ----A---P---E----P---G--IDAYVWMKPPGESDG--S----SKAID---------
ZP_04605447     ----A---P---E----P---G--IDAYVWVKPPGESDG--S----SKEIP---------
YP_288681       ----P---A---P----G------VDAYVWVKPPGESDG--A----S-------------
AAF75786        ----P---A---P----G------VDAYVWVKPPGESDG--A----S-------------
YP_001538764    ----A---P---E----P---G--IDAYVWVKPPGESDG--S----S-------------
YP_527744       ----A---P---E----P---G--VDAYVWVKPQGESDG--I----SDPNFPIDPNDPAK
NP_630629       ----P---A--------A---G--IDAYVWMKPPGESDG--S----SKLID---------
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YP_001160411    ----A---P---E----P---G--IDAYVWVKPPGESDG--S----S-------------
YP_001982934    ----P---A--------A---G--IDAYVWVKPPGESDG--V----G-------------
ZP_03817603     ----P---K---P----N------IDAYVWIKPPGESDG--S----STQIP---------
XP_002396053    ----T---G---S----S---L--IDAIVWAKPGGESDG--T----S-------------
ZP_04371165     ----T---G---V----P---L--VDADLFIKTIGESDGSCT----R-------------
AAD54679        ----V---D---D----P---L--VAGYLWIKVPGESDG--Q----CY------------
ZP_03911156     ----T---G---D----P---L--VAAYLWIKVPGESDG--L------------------
YP_871896       ----T---G---V----P---L--LDAYLWVKIPGESDG--Q----C-------------
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